

## SEQUENCE LISTING

<110> Shimkets, Richard  
Carpenter, Thomas

<120> METHODS FOR DIAGNOSING AND TREATMENT OF CONDITIONS THAT ALTER  
PHOSPHATE TRANSPORT IN MAMMALS

<130> 21402-604

<140> Not yet assigned

<141> 2003-08-20

<150> 60/404,659

<151> 2002-08-20

<150> 60/463,219

<151> 2003-04-16

<160> 6

<170> CuraSeqList version 0.1

<210> 1

<211> 606

<212> DNA

<213> Homo sapiens

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ttg ctc tac aga tca tgc ttt cac att atc tgt cta gtg ggt act ata 100  
Leu Leu Tyr Arg Ser Cys Phe His Ile Ile Cys Leu Val Gly Thr Ile  
15 20 25

tct tta gct tgc aat gac atg act cca gag caa atg gct aca aat gtg 148  
Ser Leu Ala Cys Asn Asp Met Thr Pro Glu Gln Met Ala Thr Asn Val  
30 35 40

aac tgt tcc agc cct gag cga cac aca aga agt tat gat tac atg gaa 196  
Asn Cys Ser Ser Pro Glu Arg His Thr Arg Ser Tyr Asp Tyr Met Glu  
45 50 55 60

gga ggg gat ata aga gtg aga aga ctc ttc tgt cga aca cag tgg tac 244  
Gly Gly Asp Ile Arg Val Arg Arg Leu Phe Cys Arg Thr Gln Trp Tyr  
65 70 75

ctg agg atc gat aaa aga ggc aaa gta aaa ggg acc caa gag atg aag 292  
Leu Arg Ile Asp Lys Arg Gly Lys Val Lys Gly Thr Gln Glu Met Lys  
80 85 90

aat aat tac aat atc atg gaa atc agg aca gtg gca gtt gga att gtg 340  
Asn Asn Tyr Asn Ile Met Glu Ile Arg Thr Val Ala Val Gly Ile Val  
95 100 105

gca atc aaa ggg gtg gaa agt gaa ttc tat ctt gca atg aac aag gaa 388  
Ala Ile Lys Gly Val Glu Ser Glu Phe Tyr Leu Ala Met Asn Lys Glu  
110 115 120

gga aaa ctc tat gca aag aaa gaa tgc aat gaa gat tgt aac ttc aaa 436  
Gly Lys Leu Tyr Ala Lys Lys Glu Cys Asn Glu Asp Cys Asn Phe Lys  
125 130 135 140

gaa cta att ctg gaa aac cat tac aac aca tat gca tca gct aaa tgg 484  
Glu Leu Ile Leu Glu Asn His Tyr Asn Thr Tyr Ala Ser Ala Lys Trp  
145 150 155

aca cac aac gga ggg gaa atg ttt gtt gcc tta aat caa aag ggg att 532  
Thr His Asn Gly Gly Glu Met Phe Val Ala Leu Asn Gln Lys Gly Ile  
160 165 170

cct gta aga gga aaa aaa cga aga aag aac aaa aaa cag ccc act ttc 580  
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35 40 45  
Pro Glu Arg His Thr Arg Ser Tyr Asp Tyr Met Glu Gly Gly Asp Ile  
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Arg Val Arg Arg Leu Phe Cys Arg Thr Gln Trp Tyr Leu Arg Ile Asp  
65 70 75 80  
Lys Arg Gly Lys Val Lys Gly Thr Gln Glu Met Lys Asn Asn Tyr Asn  
85 90 95  
Ile Met Glu Ile Arg Thr Val Ala Val Gly Ile Val Ala Ile Lys Gly  
100 105 110  
Val Glu Ser Glu Phe Tyr Leu Ala Met Asn Lys Glu Gly Lys Leu Tyr  
115 120 125

Ala Lys Lys Glu Cys Asn Glu Asp Cys Asn Phe Lys Glu Leu Ile Leu  
130 135 140

Glu Asn His Tyr Asn Thr Tyr Ala Ser Ala Lys Trp Thr His Asn Gly  
145 150 155 160

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caatcttcat tgcattcttt ctttgcatag agttttcctt ccttgttcat tgcaagatag 240  
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aggcaccact gtgttcgaca gaagagtctt ctactctta tatccctcc ttccatgtaa 420  
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Asn Asp Met Thr Pro Glu Gln Met Ala Thr Asn Val Asn Cys Ser Ser  
35 40 45

Pro Glu Arg His Thr Arg Ser Tyr Asp Tyr Met Glu Gly Gly Asp Ile  
50 55 60

Arg Val Arg Arg Leu Phe Cys Arg Thr Gln Trp Cys Leu Arg Ile Asp  
65 70 75 80

Lys Arg Gly Lys Val Lys Gly Thr Gln Glu Met Lys Asn Asn Tyr Asn  
85 90 95

Ile Met Glu Ile Arg Thr Val Ala Val Gly Ile Val Ala Ile Lys Gly  
100 105 110

Val Glu Ser Glu Phe Tyr Leu Ala Met Asn Lys Glu Gly Lys Leu Tyr  
115 120 125

Ala Lys Lys Glu Cys Asn Glu Asp Cys Asn Phe Lys Glu Leu Ile Leu  
130 135 140

Lys Thr Ile Thr Thr His Met His Gln Leu Asn Gly His Thr Thr Glu  
145 150 155 160

Gly Lys Cys Leu Leu Pro  
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<212> DNA  
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gctacaaatg tgaactgttc cagccctgag cgacacacaa gaagttatga ttacatggaa 180  
ggaggggata taagagttag aagactcttc tgtcgaacac agtgggtacct gaggatcgat 240  
aaaagaggca aagtaaaaagg gacccaagag atgaagaata attacaatat catggaaatc 300  
aggacagtgg cagttggaat tgtggcaatc aaaggggtgg aaagtgaatt ctatcttgca 360  
atgaacaagg aagggaaaact ctatgcaaag aaagaatgca atgaagattg taacttcaaaa 420  
gaactaatc tggaaaacca ttacaacaca tatgcatcag ctaaatggac acacaacgga 480  
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20 25 30

Asn Asp Met Thr Pro Glu Gln Met Ala Thr Asn Val Asn Cys Ser Ser  
35 40 45

Pro Glu Arg His Thr Arg Ser Tyr Asp Tyr Met Glu Gly Gly Asp Ile  
50 55 60

Arg Val Arg Arg Leu Phe Cys Arg Thr Gln Trp Tyr Leu Arg Ile Asp  
65 70 75 80

Lys Arg Gly Lys Val Lys Gly Thr Gln Glu Met Lys Asn Asn Tyr Asn  
85 90 95

Ile Met Glu Ile Arg Thr Val Ala Val Gly Ile Val Ala Ile Lys Gly  
100 105 110

Val Glu Ser Glu Phe Tyr Leu Ala Met Asn Lys Glu Gly Lys Leu Tyr  
115 120 125  
Ala Lys Lys Glu Cys Asn Glu Asp Cys Asn Phe Lys Glu Leu Ile Leu  
130 135 140  
Glu Asn His Tyr Asn Thr Tyr Ala Ser Ala Lys Trp Thr His Asn Gly  
145 150 155 160  
Gly Glu Met Phe Val Ala Leu Asn Gln Lys Gly Ile Pro Val Arg Gly  
165 170 175  
Lys Lys Thr Lys Lys Glu Gln Lys Thr Ala His Phe Leu Pro Met Ala  
180 185 190  
Ile Thr